

## SEQUENCE LISTING

&lt;110&gt; CHUGAI SEIYAKU KABUSIKI KAISHA

5 &lt;120&gt; Vascularization Inhibitors

&lt;130&gt; CGS-I 98-06 PCT

&lt;140&gt; PCT/JP99/01448

10 &lt;141&gt; 1999-03-23

&lt;150&gt; JP10/95448

&lt;151&gt; 1998-03-24

15 &lt;160&gt; 12

&lt;210&gt; 1

&lt;211&gt; 352

&lt;212&gt; PRT

20 &lt;213&gt; Mus

&lt;400&gt; 1

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	Ser Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile	
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	Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys	
	65 70	75
	Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr	
	80 85	90
35	Leu Pro Phe Trp Ala Val Asp Ala Val Ala Asn Trp Tyr Phe Gly	
	95 100	105
	Asn Phe Leu Cys Lys Ala Val His Val Ile Tyr Thr Val Asn Leu	
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	Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr	
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	Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg Lys Leu	
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	Leu Ala Glu Lys Val Val Tyr Val Gly Val Trp Ile Pro Ala Leu	
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45	Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn Val Ser Glu Ala	

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	Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr	Pro Asn Asp Leu Trp	
	185	190	195
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	Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys	Ile Ile Ile Ser Lys	
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	Leu Ser His Ser Lys Gly His Gln Lys Arg	Lys Ala Leu Lys Thr	
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10	Thr Val Ile Leu Ile Leu Ala Phe Phe Ala	Cys Trp Leu Pro Tyr	
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	Tyr Ile Gly Ile Ser Ile Asp Ser Phe Ile	Leu Leu Glu Ile Ile	
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	Ile Thr Glu Ala Leu Ala Phe Phe His Cys	Cys Leu Asn Pro Ile	
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&lt;211&gt; 1588

&lt;212&gt; DNA

30 &lt;213&gt; Mus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1059)

35

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	ctg gtc atg ggt tac cag aag aaa ctg aga agc atg acg gac aag	225
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	ctt ccc ttc tgg gca gtt gat gcc gtg gca aac tgg tac ttt ggg	315
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 20 25 30  
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 35 40 45  
 Ile Tyr Phe Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu  
 50 55 60  
 40 Val Ile Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr  
 65 70 75  
 Asp Lys Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val  
 80 85 90  
 Ile Thr Leu Pro Phe Trp Ala Val Asp Ala Met al.a Asp Trp Tyr  
 45 95 100 105

	Phe Gly Lys Phe Leu Cys Lys Ala Val His Ile Ile Tyr Thr Val	
	110 115	120
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5	Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg	
	140 145	150
	Lys Leu Leu Ala Glu Lys Ala Val Tyr Val Gly Val Trp Ile Pro	
	155 160	165
	Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asp Val Ser	
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	Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile Cys Asp Arg	
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	Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe Gln His	
	200 205	210
15	Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser Cys	
	215 220	225
	Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln	
	230 235	240
	Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe	
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	Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser	
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	290 295	300
	His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys	
	305 310	315
	Phe Lys Ser Ser Ala Gln His Ala Leu Asn Ser Met Ser Arg Gly	
30	320 325	330
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 gtg atc ctg gtc atg ggt tac cag aag aag cta agg agc atg acg 225  
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 atc aca ctc ccc ttc tgg gca gtt gat gcc atg gct gac tgg tac 315  
 ttt ggg aaa ttt ttg tgt aag gct gtc cat atc atc tac act gtc 360  
 10 aac ctc tac agc agc gtt ctc atc ctg gcc ttc atc agc ctg gac 405  
 cgg tac ctc gcc att gtc cac gcc acc aac agt caa agg cca agg 450  
 aaa ctg ctg gct gaa aag gca gtc tat gtg ggc gtc tgg atc cca 495  
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 cag ggg gac atc agt cag ggg gat gac agg tac atc tgt gac cgc 585  
 15 ctt tac ccc gat agc ctg tgg atg gtg gtg ttt caa ttc cag cat 630  
 ata atg gtg ggt ctc atc ctg ccc ggc atc gtc atc ctc tcc tgt 675  
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1758

&lt;210&gt; 5

40 &lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;223&gt; Ligand peptide

45

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Pro Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys  
35 40 45  
His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val  
50 55 60  
10 Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys  
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ctc tgc ctc agc gac ggg aag ccc gtc agc ctg agc tac aga tgc 563  
35 cca tgc cga ttc ttc gaa agc cat gtt gcc aga gcc aac gtc aag 608  
cat ctc aaa att ctc aac act cca aac tgt gcc ctt cag att gta 653  
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25 <223> Ligand peptide

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 35 35 40 45  
 His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val  
 50 55 60  
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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (82)...(351)

5

&lt;400&gt; 8

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10

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ccc tgc cgg ttc ttc gag agc cac atc gcc aga gcc aac gtc aag 216

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gca cgg ctg aag aac aac aac aga caa gtg tgc att gac ccg aaa 306

tta aag tgg atc caa gag tac ctg gag aaa gct tta aac aag taa 351

15

gcacaacagc ccaaaggact ttccagtaga ccccgagga aggctgacat ccgtgggaga 411

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aaacttgcac acattcttat gatcacagac ggccctgggtg gtttttggtg actatttaca 1491

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&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

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&lt;220&gt;



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